

FIGURE 1

Page 1

FIGURE 2A

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FIGURE 2A

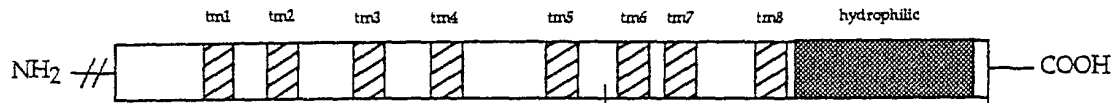
SECRET

Translation of full length pmt cDNA

1	MASRGARQRL	KGSGASSGDT	APAADKLREL	LGSREAGGAE	HRTELSGNKA
51	GQVWAPGST	AFKCLLSARL	CAALLSNISD	CDEFNYWEP	THYLIYGEGF
101	QTWEYSPAYA	IRSYAYLLLH	AWPAAFHARI	LQTNKILVfy	FLRCLLAFVS
151	CICELYFYKA	VCKKFGLHVS	RMMLAFLVLS	TGMFCSSSAF	LPSSFECMYTT
201	LIAMTGWYMD	KTSIAVLGVA	AGAILGWPFs	AALGLPIAFD	LLVMKHRWKS
251	FFHWSLMALI	LELVFVVVID	SYYYGKLVIA	PLNIVLYNVF	TPHGPDLYGT
301	EPWYFYLING	FLNFNVAFAL	ALLVLPLTSL	MEYLLQRFHV	QNLGHPYWLT
351	LAPMYIWFII	FFIQPHKEER	FLFPVYPLIC	LCGAVALSAL	QKCYHFVFQR
401	YRLEHYTVTS	NWLALGTVFL	FGLLSFSRSV	ALFRGYHGPL	DLYPEFYRIA
451	TDPTIHTVPE	GRPVNVCVGK	EWYRFPSSEL	LPDNWQLQFI	PSEFRGQLPK
501	PFAEGPLATR	IVPTDMNDQN	LEEPSRYIDI	SKCHYLVLDL	TMRETPREPK
551	YSSNKEEWIS	LAYRPFLDAS	RSSKLLRAFY	VPFLSDQYTV	YVNYTILKPR
601	KAKQIRKKSG	G			

Schematic of Fusion Open Reading Frame

putative Mannose Transferase



CGTACAATGTGAAGAAAGTCCTTGTAACCTT 31
CGCCTTCCGCCATAATGGCAGGGGCATCCAGTGGTTCAAGGTTACAATAAGCTGTGATCGTGCCACTGCATTCTACCTGGG 112

1 M T E W D P V P Q S E T L S Q K K K L C K S K E T T S
ATGACAGAGTGGGACCCTGTGCCACAGAGTGAGACCCTGTCTCAAAAAAAAAAACTATGTAAATCCAAGGAGACGACTTCA 193
28 P V L Y L S K F W K V D G G F T Q N F N L S R T E F C
CCTGTATTGTACCTCTCCAAGTTCTGGAAAGTCGATGGAGGGTTTACTCAGAACTTCAATCTATCCAGAACTGAGTTTGT 274

Fusion Partner

55 L W C V P
TTATGGTGTGTGCCAG 290
CTGCAGAGATTTTCATGTTTCAGAATTTAGGCCACCCGATTGGCTTACCTTGGCTCCAATGTATATTTGGTTTATAATTTTC 355
V Q N L G H P Y W L T L A P M Y I W F I I F

Exon 7* Exon 8*

TTCATCCAGCCTCACAAGAGGAGAGATTTCTTTTCCCTGTGTATCCACTTATATGTCTCTGTGGCGCTGTGGCTCTCTCT 436
82 F I Q P H K E E R F L F P V Y P L I C L C G A V A L S
GCACCTCAGAAATGTTACCACTTTGTGTTTCAACGATATCGCCTGGAGCACTATACTGTGACATCGAATTGGCTGGCATT 517
109 A L Q K C Y H F V F Q R Y R L E H Y T V T S N W L A L
GGAAGTGTCTTCTGTTTGGGCTCTTGTCTTCTCGCTCTGTGGCACTGTTTCAGAGGATATCACGGGCCCTTGATTG 598
136 G T V F L F G L L S F S R S V A L F R G Y H G P L D L
TATCCAGAATTTTACCGAATTGCTACAGACCCCAACCATCCACACTGTCCAGAAAGGCAGACCTGTGAATGTCTGTGTGGGA 679
163 Y P E F Y R I A T D P T I H T V P E G R P V N V C V G
AAAGAGTGGTATCGATTTCCAGCAGCTTCTTCTCTCTGACAATTGGCAGCTTCAGTTCATTCCATCAGAGTTCAGAGGT 760
190 K E W Y R F P S S F L L P D N W Q L Q F I P S E F R G
CAGTTACCAAAACCTTTTGCAGAAGGACCTCTGGCCACCCGGATTGTTCTACTGACATGAATGACCAGAATCAGAAGAGC 841
217 Q L P K P F A E G P L A T R I V P T D M N D Q N Q K S
CATCCAGATATATTGATATCAGTAAATGCCATTATTAG 880
243 H P D I L I S V N A I I .

Partner - putative Mannose Transferase fusion

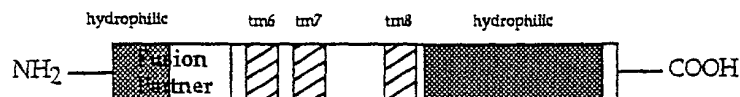


FIGURE 3

PUTATIVE MANNOSYL TRANSFERASE 5'-FUSION TRANSCRIPT

CGTACAATGTGAAGAAAGTCCTTGTACCCCTTGGCCTTCCGCCATAATGGCAGGGGCATCCAGTGGTTCAAGGTTACAATA

AGCTGTGATCGTGCCACTGCATTCTAOCCTGGGATGACAGAGTGGGAOCCTGTGCCACAGAGTGAGACOCCTGTCTCAAAAA

M T E W D P V P Q S E T L S Q K

AAAAAACTATGTAAATCCAAGGAGACGACTTCACCTGTATTGTACCTCTCCAAGTTCTGGAAAGTCGATGGAGGGTTTAC

K K L C K S K E T T S P V L Y L S K F W K V D G G F T

CAGAACTTCAATCTATCCAGAACTGAGTTTTGTTTATGGTGTGTGCCAGTTCAGAATTTAGGCCACCCGATTGGCTTA

Q N F N L S R T E F C L W C V P

CCTTGGCTCCAATGTATATTTGGTTTATAATTTCTTCATCCAGCCTCACAAAGAGGAGAGATTTCTTTTCCCTGTGTAT
CCACTTATATGTCTCTGTGGCGCTGTGGCTCTCTCTGCACTTCAGAAATGTTACCACTTTGTGTTTCAAAGATATGGCCT
GGAGCACTATACTGTGACATCGAATTGGCTGGCATTAGGAACTGTCTTCTGTGTTGGGCTCTTGTCAATTTCTGGCTCTG
TGGCACTGTTTCAAGGATATCACGGGCCCCCTTGATTTGTATCCAGAATTTTACCGAATTGCTACAGACCCCAACCATOCAC
ACTGTCCAGAAGGCAGACCTGTGAATGTCTGTGTGGGAAAAGAGTGGTATCGATTTCCAGCAGCTTCTCTTCTCTGA
CAATTGGCAGCTTCAGTTCATTCCATCAGAGTTCAGAGGTCAGTTACCAAAACCTTTTGCAGAAGGACCTCTGGCCACCC
GGATTGTTCTACTGACATGAATGACCAGAATCAGAAGAGCCATCCAGATATATTGATATCAGTAAATGOCATTATTTAG
TGGATTTGGACAOCATGAGAGAAACACCCCGGGAGCCAAAATATTCATCCAATAAAGAAGAATGGATCAGCTTGGCCTAT
AGACCATTCCTTGATGCTTCTAGATCTTCAAAGCTGCTGCGGGCATTCTATGTCCCTTCTGTGATCAGTATACAGT
GTACGTAAACTACAOCATCCTCAAACCCCGGAAAGCAAAGCAAATCAGGAAGAAAAGTGGAGGTTAGCAACACAOCCTGTG
GCCCCAAAGGACAACCATCTTGTTAACTATTGATTCCAGTGACCTGACTCCCTGCAAGTCATGGCCTGTAAACATTGTAA
AAAGGTCTTCTGACATGAAAAAAAAA

FIGURE 4

Putative Fusion protein chr 11/9

```

      NcoI
      ~~~~~
      Met AlaSerArg GlyAlaArg GlnArgLeuLys GlySerGly·
1      A TGGCTAGTCG AGGGGCTCGG CAGCGCCTGA AGGGCAGCGG
      T ACCGATCAGC TCCCCGAGCC GTCGCGGACT TCCCGTCGCG
      ~~~~~
      ~~~~~
51      ·AlaSerSer GlyAspThrAla ProAlaAla AspLysLeu ArgGluLeuLeu·
      GGCCAGCAGT GGGGATACGG CCCC GGCTGC GGACAAGCTG CGGGAGCTGC
      CCGGTCGTCA CCCCTATGCC GGGGCCGACG CCTGTTCGAC GCCCTCGACG
      ~~~~~
      ~~~~~
101      ·LGlySerArg GluAlaGly GlyAlaGluHis ArgThrGlu LeuSerGly
      TGGGCAGCCG AGAGGCGGGC GCGCGGAGC ACCGGACCGA GTTATCTGGG
      ACCCGTCGGC TCTCCGCCCG CCGCGCCTCG TGGCCTGGCT CAATAGACCC
      ~~~~~
      ~~~~~
151      AsnLysAlaGly GlnValTrp AlaProGlu GlySerThrAla PheLysCys·
      AACAAAGCAG GACAAGTCTG GGCACCTGAA GGATCTACTG CTTTCAAGTG
      TTGTTTCGTC CTGTTCAGAC CCGTGGACTT CCTAGATGAC GAAAGTTCAC
      ~~~~~
      ~~~~~
201      ·LeuLeuSer AlaArgLeuCys AlaAlaLeu LeuSerAsn IleSerAspCys·
      TCTGCTTTCA GCAAGGTTAT GTGCTGCTCT CCTGAGCAAC ATCTCTGACT
      AGACGAAAGT CGTTCCAATA CACGACGAGA GGACTCGTTG TAGAGACTGA
      ~~~~~
      ~~~~~
251      ·CAspGluThr PheAsnTyr TrpGluProThr HisTyrLeu IleTyrGly
      GTGATGAAAC ATTCAACTAC TGGGAGCAA CACACTACCT CATCTATGGG
      CACTACTTTG TAAGTTGATG ACCCTCGGTT GTGTGATGGA GTAGATACCC
      ~~~~~
      ~~~~~
301      GluGlyPheGln ThrTrpGlu TyrSerPro AlaTyrAlaIle ArgSerTyr·
      GAAGGGTTTC AGACTTGGA ATATTCCCA GCATATGCCA TTCGCTCCTA
      CTTCCCAAAG TCTGAACCCT TATAAGGGGT CGTATACGGT AAGCGAGGAT
      ~~~~~
      ~~~~~
      EcoRI
      ~~~~~
      ~~~~~
351      ·AlaTyrLeu LeuLeuHisAla TrpProAla AlaPheHis AlaArgIleLeu·
      TGCTTACCTG TTGCTTCATG CCTGGCCAGC TGCATTTTCAT GCAAGAATTC
      ACGAATGGAC AACGAAGTAC GGACCGGTCG ACGTAAAGTA CGTTCTTAAG
      ~~~~~
      ~~~~~
401      ·LGlnThrAsn LysIleLeu ValPheTyrPhe LeuArgCys LeuLeuAla
      TACAAACTAA TAAGATTCTT GTGTTTTACT TTTTGCGATG TCTTCTGGCT
      ATGTTTGATT ATTCTAAGAA CACAAAATGA AAAACGCTAC AGAAGACCGA
      ~~~~~
      ~~~~~
451      PheValSerCys IleCysGlu LeuTyrPhe TyrLysAlaVal CysLysLys·
      TTTGTGAGCT GTATTTGTGA ACTTTACTTT TACAAGGCTG TGTGCAAGAA
      AAACACTCGA CATAAACAAT TGAAATGAAA ATGTTCCGAC ACACGTTCTT
      ~~~~~
      ~~~~~
501      ·PheGlyLeu HisValSerArg MetMetLeu AlaPheLeu ValLeuSerThr·
      GTTTGGGTTG CACGTGAGTC GAATGATGCT AGCCTTCTTG GTTCTCAGCA
      CAAACCCAAC GTGCACTCAG CTTACTACGA TCGGAAGAAC CAAGAGTCGT

```

FIGURE 5


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~~~~~
551  •TGLyMetPhe CysSerSer SerAlaPheLeu ProSerSer PheCysMet
    CTGGCATGTT TTGCTCATCA TCAGCATTCC TTCCTAGTAG CTTCTGTATG
    GACCGTACAA AACGAGTAGT AGTCGTAAGG AAGGATCATC GAAGACATAC
    ~~~~~
601  TyrThrThrLeu IleAlaMet ThrGlyTrp TyrMetAspLys ThrSerIle•
    TACACTACGT TGATAGCCAT GACTGGATGG TATATGGACA AGACTTCCAT
    ATGTGATGCA ACTATCGGTA CTGACCTACC ATATACCTGT TCTGAAGGTA
    ~~~~~
651  •AlaValLeu GlyValAlaAla GlyAlaIle LeuGlyTrp ProPheSerAla•
    TGCTGTGCTG GGAGTAGCAG CTGGGGCTAT CTTAGGCTGG CCATTCACTG
    ACGACACGAC CCTCATCGTC GACCCCGATA GAATCCGACC GGTAAGTCAC
    ~~~~~
701  •AAlaLeuGly LeuProIle AlaPheAspLeu LeuValMet LysHisArg
    CAGCTCTTGG TTTACCCATT GCCTTTGATT TGCTGGTCAT GAAACACAGG
    GTCGAGAACC AAATGGGTAA CGGAAACTAA ACGACCAGTA CTTTGTGTCC
    ~~~~~
751  TrpLysSerPhe PheHisTrp SerLeuMet AlaLeuIleLeu PheLeuVal•
    TGGAAGAGTT TCTTTCATTG GTCGCTGATG GCCCTCATAC TATTTCTGGT
    ACCTTCTCAA AGAAAGTAAC CAGCGACTAC CGGGAGTATG ATAAAGACCA
    801  •ProValVal ValIleAspSer TyrTyrTyr GlyLysLeu ValIleAlaPro•
    GCCTGTGGTG GTCATTGACA GCTACTATTA TGGGAAGTTG GTGATTGCAC
    CGGACACCAC CAGTAACTGT CGATGATAAT ACCCTTCAAC CACTAACGTG
    851  •PLeuAsnIle ValLeuTyr AsnValPheThr ProHisGly ProAspLeu
    CACTCAACAT TGTTTTGTAT AATGTCTTTA CTCCTCATGG ACCTGATCTT
    GTGAGTTGTA ACAAACATA TTACAGAAAT GAGGAGTACC TGGACTAGAA
    901  TyrGlyThrGlu ProTrpTyr PheTyrLeu IleAsnGlyPhe LeuAsnPhe•
    TATGGTACAG AACCCTGGTA TTTCTATTTA ATTAATGGAT TTCTGAATTT
    ATACCATGTC TTGGGACCAT AAAGATAAAT TAATTACCTA AAGACTTAAA
    951  •AsnValAla PheAlaLeuAla LeuLeuVal LeuProLeu ThrSerLeuMet•
    CAATGTAGCC TTTGCTTTGG CTCTCCTAGT CCTACCACTG ACTTCTCTTA
    GTTACATCGG AAACGAAACC GAGAGGATCA GGATGGTGAC TGAAGAGAAT
    PstI
    ~~~~~
1001 •MGLuTyrLeu LeuGlnArg PheHis
    TGGAATACCT GCTGCAGAGA TTTCATG
    ACCTTATGGA CGACGTCTCT AAAGTAC

```

FIGURE 5

Putative fusion protein 9/11

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1   CGTACAATGT GAAGAAAGTC CTTGTACCCT TCGCCTTCCG CCATAATGGC
   GCATGTTACA CTTCTTTTCAG GAACATGGGA AGCGGAAGGC GGTATTACCG
51  AGGGGCAATC CAGTGGTTCA AGGTTACAAT AAGCTGTGAT CGTGCCACTG
   TCCCCGTTAG GTCACCAAGT TCCAATGTTA TTCGACACTA GCACGGTGAC
   MetThrGlu TrpAspPro ValProGln SerGluThrLeu·
   ~~~~~

101  CATTCTACCT GGGATGACAG AGTGGGACCC TGTGCCACAG AGTGAGACCC
   GTAAGATGGA CCCTACTGTC TCACCCTGGG ACACGGTGTC TCACTCTGGG
   ·LSerGlnLys LysLysLeu CysLysSerLys GluThrThr SerProVal
   ~~~~~

151  TGTCTCAAAA AAAAAAATA TGTAATCCA AGGAGACGAC TTCACCTGTA
   ACAGAGTTTT TTTTTTTGAT ACATTTAGGT TCCTCTGCTG AAGTGGACAT
   LeuTyrLeuSer LysPheTrp LysValAsp GlyGlyPheThr GlnAsnPhe·
   ~~~~~

201  TTGTACCTCT CCAAGTTCTG GAAAGTCGAT GGAGGGTTTA CTCAGAACTT
   AACATGGAGA GGTTCAAGAC CTTTCAGCTA CCTCCCAAAT GAGTCTTGAA
   ·AsnLeuSer ArgThrGluPhe CysLeuTrp CysValPro   GlnAsnLeu·
   ~~~~~

251  CAATCTATCC AGAACTGAGT TTTGTTTATG GTGTGTGCCA GTTCAGAATT
   GTTAGATAGG TCTTGACTCA AAACAAATAC CACACACGGT CAAGTCTTAA
   ·LGlyHisPro TyrTrpLeu ThrLeuAlaPro MetTyrIle TrpPheIle
   ~~~~~

301  TAGGCCACCC GTATTGGCTT ACCTTGCTC CAATGTATAT TTGGTTTATA
   ATCCGGTGGG CATAACCGAA TGGAAACCGAG GTTACATATA AACCAAATAT
   ~~~~~
   IlePhePheIle GlnProHis LysGluGlu ArgPheLeuPhe ProValTyr·
   ~~~~~

351  ATTTTCTTCA TCCAGCCTCA CAAAGAGGAG AGATTTCTTT TCCCTGTGTA
   TAAAAGAAGT AGGTCGGAGT GTTCTCCTC TCTAAAGAAA AGGGACACAT
   ~~~~~
   ·ProLeuIle CysLeuCysGly AlaValAla LeuSerAla LeuGlnLysCys·
   ~~~~~

401  TCCACTTATA TGTCTCTGTG GCGCTGTGGC TCTCTCTGCA CTTCAGAAAT
   AGGTGAATAT ACAGAGACAC CGCGACACCG AGAGAGACGT GAAGTCTTTA
   ~~~~~
   ·CTyrHisPhe ValPheGln ArgTyrArgLeu GluHisTyr ThrValThr
   ~~~~~

451  GTTACCACTT TGTGTTTCAA CGATATCGCC TGGAGCACTA TACTGTGACA
   CAATGGTGAA ACACAAAGTT GCTATAGCGG ACCTCGTGAT ATGACACTGT
   ~~~~~
   SerAsnTrpLeu AlaLeuGly ThrValPhe LeuPheGlyLeu LeuSerPhe·
   ~~~~~

501  TCGAATTGGC TGGCATTAGG AACTGTCTTC CTGTTTGGGC TCTTGTCATT

```

FIGURE 6

```

AGCTTAACCG ACCGTAATCC TTGACAGAAG GACAAACCCG AGAACAGTAA
~~~~~
•SerArgSer ValAlaLeuPhe ArgGlyTyr HisGlyPro LeuAspLeuTyr•
~~~~~
551 TTCTCGCTCT GTGGCACTGT TCAGAGGATA TCACGGGCCC CTTGATTGT
AAGAGCGAGA CACCGTGACA AGTCTCCTAT AGTGCCCGGG GAACTAAACA
~~~~~
•TProGluPhe TyrArgIle AlaThrAspPro ThrIleHis ThrValPro
~~~~~
601 ATCCAGAATT TTACCGAATT GCTACAGACC CAACCATCCA CACTGTCCCA
TAGGTCTTAA AATGGCTTAA CGATGTCTGG GTTGGTAGGT GTGACAGGGT
                               ClaI
                               ~~~~~
GluGlyArgPro ValAsnVal CysValGly LysGluTrpTyr ArgPhePro•
~~~~~
651 GAAGGCAGAC CTGTGAATGT CTGTGTGGGA AAAGAGTGGT ATCGATTTC
CTTCCGTCTG GACACTTACA GACACACCCT TTTCTCACC TAGCTAAAGG
•SerSerPhe LeuLeuProAsp AsnTrpGln LeuGlnPhe IleProSerGlu•
~~~~~
701 CAGCAGCTTC CTTCTTCCTG ACAATTGGCA GCTTCAGTTC ATTCCATCAG
GTCGTGCAAG GAAGAAGGAC TGTTAACCGT CGAAGTCAAG TAAGGTAGTC
•GPheArgGly GlnLeuPro LysProPheAla GluGlyPro LeuAlaThr
~~~~~
751 AGTTCAGAGG TCAGTTACCA AAACCTTTTG CAGAAGGACC TCTGGCCACC
TCAAGTCTCC AGTCAATGGT TTTGGAAAC GTCTTCCTGG AGACCGGTGG
ArgIleValPro ThrAspMet AsnAspGln AsnLeuGluGlu ProSerArg•
~~~~~
801 CGGATTGTTC CTACTGACAT GAATGACCAG AATCTAGAAG AGCCATCCAG
GCCTAACAAG GATGACTGTA CTTACTGGTC TTAGATCTTC TCGGTAGGTC
•TyrIleAsp IleSerLysCys HisTyrLeu ValAspLeu AspThrMetArg•
~~~~~
851 ATATATTGAT ATCAGTAAAT GCCATTATT AGTGGATTG GACACCATGA
TATATAACTA TAGTCATTTA CGGTAATAAA TCACCTAAAC CTGTGGTACT
      SmaI
      ~~~~~
      XmaI
      ~~~~~
      AvaI
      ~~~~~
•AGluThrPro ArgGluPro LysTyrSerSer AsnLysGlu GluTrpIle
~~~~~
901 GAGAAACACC CCGGGAGCCA AAATATTCAT CCAATAAAGA AGAATGGATC
CTCTTTGTGG GGCCCTCGGT TTTATAAGTA GGTATTCTCT TCTTACCTAG
SerLeuAlaTyr ArgProPhe LeuAspAla SerArgSerSer LysLeuLeu•
~~~~~
951 AGCTTGGCCT ATAGACCATT CCTTGATGCT TCTAGATCTT CAAAGCTGCT
TCGAACCGGA TATCTGGTAA GGAACACGA AGATCTAGAA GTTTCGACGA
•ArgAlaPhe TyrValProPhe LeuSerAsp GlnTyrThr ValTyrValAsn•
~~~~~
1001 GCGGGCATTTC TATGTCCCCT TCCTGTCAGA TCAGTATACA GTGTACGTAA
CGCCCCGAAG ATACAGGGGA AGGACAGTCT AGTCATATGT CACATGCATT
•ATyrThrIle LeuLysPro ArgLysAlaLys GlnIleArg LysLysSer

```

FIGURE 6

09222650

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~~~~~  
1051  ACTACACCAT CCTCAAACCC CGGAAAGCAA AGCAAATCAG GAAGAAAAGT  
      TGATGTGGTA GGAGTTTGGG GCCTTTCGTT TCGTTTAGTC CTTCTTTTCA  
      GlyGly  
      ~~~~~  
1101  GGAGGTTAGC AACACACCTG TGGCCCCAAA GGACAACCAT CTTGTAACT  
      CCTCCAATCG TTGTGTGGAC ACCGGGGTTT CCTGTTGGTA GAACAATTGA  
1151  ATTGATTCCA GTGACCTGAC TCCCTGCAAG TCATCGCCTG TAACATTGT  
      TAACTAAGGT CACTGGACTG AGGGACGTTT AGTAGCGGAC ATTGTAAACA  
1201  AATAAAGGTC TTCTGACATG AAAAA  
      TTATTTCCAG AAGACTGTAC TTTTT
```

FIGURE 6

FIGURE 6

Chromosome 9 est (gene) involved in fusion:

```

1      AGCGGGTGGG CGCGAGTCGG CCTCCCGCGG TGCCGCCGCA GCGTGGCGCG
      TCGCCACCCC GCGCTCAGCC GGAGGGCGCC ACGGCGGCGT CGCACC GCGC
51     GAGAGGCAGG GGCATCCAGT GGTTC AAGGT TACAATAAGC TGTGATCGTG
      CTCTCCGTCC CCGTAGGTCA CCAAGTTCCA ATGTTATTCG ACCTAGCAC
                                           Glu•
                                           ~~~
101    CCACTGCATT CTACCTGGGA TGACAGAGTG GGACCCTGTG CCACAGAGTG
      GGTGACGTAA GATGGACCTT ACTGTCTCAC CCTGGGACAC GGTGTCTCAC
      •GThrLeuSer GlnLysLys LysLysLeuCys LysSerLys LysLysArg
      ~~~~~
151    AGACCCTGTC TCAAAAAAAA AAAAACTAT GTAAATCCAA GAAAAAAGA
      TCTGGGACAG AGTTTTTTTT TTTTGTGATA CATTTAGGTT CTTTTTTTCT
      LysGlnLeuLeu TrpProPhe AlaSerHis ProGluArgVal SerIleGly•
      ~~~~~
201    AAACAGCTCC TGTGGCCTTT TGCCTCTCAT CCAGAAAGGG TATCCATTGG
      TTTGTGCGAGG ACACCGGAAA ACGGAGAGTA GGTCTTTCCC ATAGGTAACC
      •LeuSerAsn IleSerSerSer CysGlnAla ThrAsnGly AspAspProPro•
      ~~~~~
251    CCTTTCTAAT ATCTCTTCAT CCTGTCAGGC CACAAATGGA GACGACCCAC
      GGAAAGATTA TAGAGAAGTA GGACAGTCCG GTGTTTACCT CTGCTGGGTG
      •PValTrpTyr LeuSerLys PheTrpLysVal AspGlyGly PheThrGln
      ~~~~~
301    CTGTATGGTA CCTCTCCAAG TTCTGGAAAG TCGATGGAGG GTTTACTCAG
      GACATACCAT GGAGAGGTTC AAGACCTTTC AGCTACCTCC CAAATGAGTC
      AsnPheAsnLeu SerArgThr GluPheGly LysTrpCysVal ProGlyArg•
      ~~~~~
351    AACTTCAATC TATCCAGAAC TGAGTTTGGT AAATGGTGTG TGCCAGGCAG
      TTGAAGTTAG ATAGGTCTTG ACTCAAACCA TTTACCACAC ACGGTCCGTC
                                           EcoRI
                                           ~~~~~
      •GlyLeuAsn SerSerAlaTyr HisTrpAla GluValThr GlyIleGlnGlu•
      ~~~~~
401    GGGATTAAAC AGTAGTGCAT ATCACTGGGC TGAAGTGACA GGAATTCAAG
      CCCTAATTTG TCATCACGTA TAGTGACCCG ACTTCACTGT CCTTAAGTTC
      •GGlnAsnAla SerThrPro ProValSerLeu SerCysLeu PheLeuLeu
451    AACAGAATGC ATCCACTCCT CCAGTCTCAT TAAGCTGCCT CTTTCTACTG
      TTGTCTTACG TAGGTGAGGA GGTCAGAGTA ATTCGACGGA GAAAGATGAC
      LysTrpArgTrp GlyPheGln AspThrSer GlnProThrGly ThrThrGly•
501    AAATGGCGAT GGGGATTCCA GGACACCTCT CAACCTACAG GAACCACTGG
      TTTACCGCTA CCCCTAAGGT CCTGTGGAGA GTTGGATGTC CTTGGTGACC
      •Ser
551    ATCTAA
      TAGATT

```

T0260-0304

FIGURE 7

FIGURE 8. Sequences of mannosyl transferase proteins.

Human (SEQ ID NO: 2) (100%)

1 masrgarqrl kgsqassgdt apaadklrel lgsreaggae hrtelsnka qqvwapegst
61 afkcillsarl caallsnisd cdefnywep thyliyggegf qtweyspaya irsyaylllh
121 awpaafhari lqtnkilvfy flrcllafvs cicelyfyka vckkfghlvs rmmalafvlvs
181 tgmfcsssaf lpssfcmytt liamtgwymd ktsiavlgva agailgw pfs aalgpliafd
241 llvmkhrwks ffhwsmlali lflvpvvid syyygklvia plnivlynvf tphgpdlygt
301 epwyfying flnfnvafal allvpltsl meyllqrhfv qnlghpywlt lapmyiwfii
361 ffiqphkeer flfpvyplic lcgavalsal qkcyhfvfqr yrlehytvts nwlalgtvfl
421 fgllsfersv alfrgyhgpl dlypefyria tdptihtvpe grpvnvcvgk ewyrfpssfl
481 lpdnwqlqfi psefgrqlpk pfaegplatr ivptdmndqn leepsryidi skchylvdld
541 tmretprepk yssnkeewis layrpfldas rsskllrafy vpflsdqyvt yvnytilkpr
601 kakqirkksg g

S. cerevisiae (ALG9) (SEQ ID NO:11) (33.1%)

mposkprksl svsfvwtfsi lavlrtsas frviddcdev ynyweplyhl lygyglqtwe
yspeyairsw fyialhavpg flarglglr lhvfyrfirgv lacfsafcet nlilavarnf
nravalhlts vlfvnsqmw s astsflpssf amnmvtlals aqlspstkr tvkvvsfity
gavigwpfsa alsipfille lvdikgrfrh lfcwfkaf vallitgici tvdslyfhyri
qfvawnivky nvlakdgrgp diygteppwy yfanlsqhn ivlwfamacg plvllaafn
winldsflldl ssvispfyiw lfifiiqphk eerfmypiyp vlclaaaigl dmslklmiqi
lssinetvrs kfpvrffvvc vyaiigclsi arilainyn apmiiypais fletdnnvt
nvcvgkewyr ypstfflpdn srlkfvksef dgilpgefe snstwwnreg yyqiheimne
fnneetryt slescdflid lefdhskatv nepiysksdg wipvmvypfi dtkqtpfmg
afavpfiepk wgryeilvkk pvkidfsnlr raskqqa

Arabidopsis (SEQ ID NO: 12) (31.2 %)

mdltttrqrr plisdsssss stksysktdk pgrsnggdae dgglrwflpf ialcylryms
atsniihdcd evfnyweply yilyksgfqt weyssnfalr syllylfhel agrpaswwfg
ddkvrvfayv rlfglvsv sdtvlvvals rkygkriaty avamlcltsg cffastsflp
ssfsmyaisl ssglllfeky amavavsvvg vilgw pfsil aflpvviysl vkrfkqafia
gavttifilg vsllvdyyyy krwtssvlnl liynvlggge shlygtagal fyirngfnnf
nfcfilamlf vaiypvirrk ydrallvvis pmyiwlafms lqphkeerfl ypiyplivcs
asavienipe lfreykssre silvtitkym rpvilgcilc ashstfali ngysaplevy
kllchddag pgsvlcvgse whrypsffv phyisevrwi ddgfrgllpf pfnntlsgts
aspyfnnkn qaseeqylkn ietctfliel qlsrpyqyrg sdlistweaia vlpdyldrels
pakyrffip hmqeknvfg kyvalrrvpk

C. elegans (SEQ ID NO: 13) (33.1%)

mvthrrkgs gppqkpppri vdrssfdadk kkikveklyh kannpdndwp fsfgsvfkml
lsirisgaiw giindcdevy nyweplyhlfl ygegfqtwey spvyairsyf yiylhyipas
lfanlfgdtk ivvftlirlt iglfcollgey yafdaickki niatgrffil fsifssgmfl
astafvpssf cmaityfilg aylnenwtg ifcvafstmv gwpfsavlgp pivadmlllk
glrirfils lviglciggy qvitdshyfg ktvlaplnif lynvvsqpgp slygeeplyf
yiknlfnnwn ivifaapfgv plslayftkv wmsqdrnval yqrfapiill avttaawlli
fgsqahkeer flfpiypfia ffaalaldat nrlclkklgm dnlsilfil cfailsasrt
ysihnnysgh veiyrslae ltnrtfnknf hdpirvcvgk ewhrfpssff ipqtvsdgkk
vemrfiqsef rgllpkpflk scklvevtrh iptemnnlq eeisryvdld scdyvvdvdm
pqsdrepdfr kmrqnykrkt kkkwkriena ilqfwlnslf eeikflnsnf hsfpffffvd
nfglfqaysh ysflkitgnq wirfhssmsp nqgdsmsgffv hfmfhsflpn ims

FIGURE 8

D. melanogaster (SEQ ID NO: 14) (40.6%)

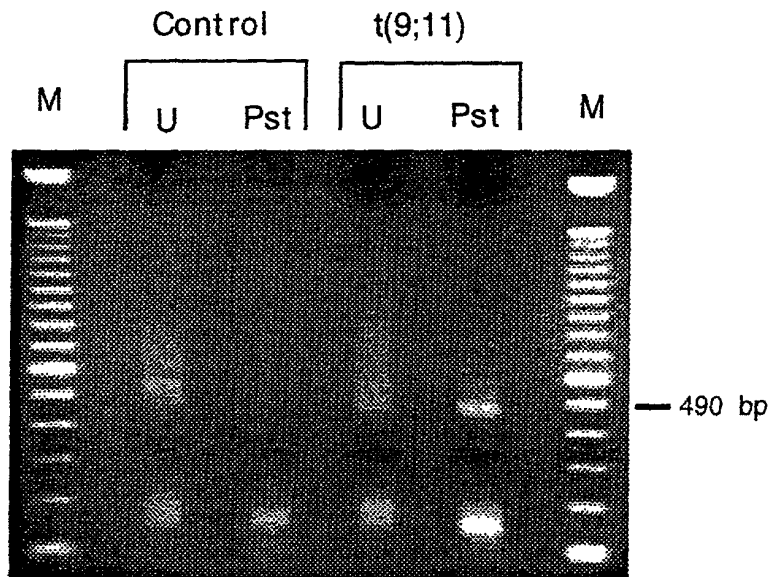
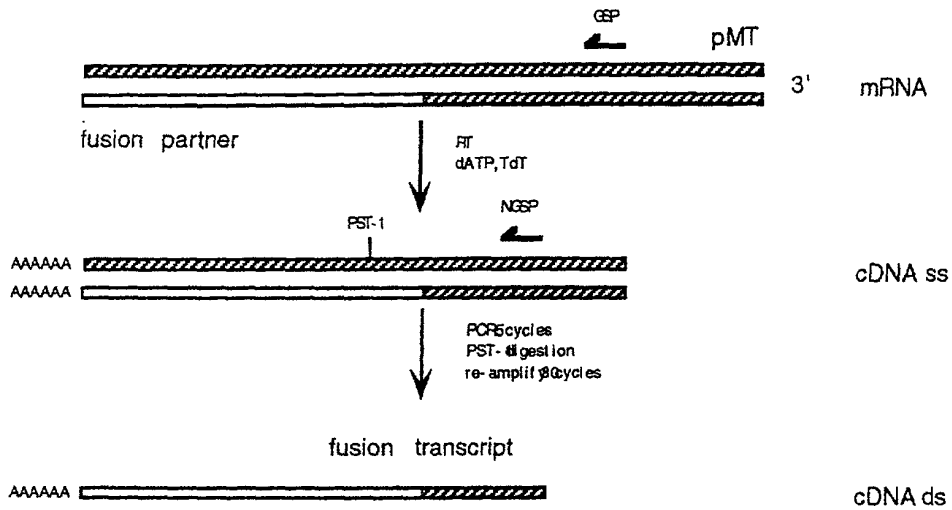
mappaarary iankadnqil skkppkrpgl ngnnktkeat pagkkkdka kkrnqptsgg
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spqfglrst ylllqgvpgy fyqklfnpsp ilifymvrcm lgfgcavmer ymyksicqef
gihigrwlwli fqlfsvgmfv sstallpssf smyfgcaala awwqgnycfa ifltaisall
gwpfaaligi plvlemlrlq rdwktfvqwt lisgatvaip miaidtsyfg kltfaplniv
wynvftshgp nifgteplsy yiingflnfn iiwllalqlp imlvidyliv pakskstlnf
physislaply lwllvffaqp hkeerflfpi yplislcgai tvdvyqriff rmksvvfkik
agvhyldhsm fiailmvmts tllglsvrfa lyrnyhapmd lmlelnqfka tpqydpdviy
nvcigkdwhr ypgsfffpak nfrlrflkse frgmipayyd egqnatkvvq pyfndlnqen
ehmyfdydrd dflvdfdegk ytalepnysk rskdwsvmks lpflipeksh kvlrafyvpf
ltdnhiqygd fnllkrktkr ngr

S. pombe (SEQ ID NO: 15) (33.1%)

mpskaprksl svsfvwtfsi lavlrlltsas frviddcdev ynyweplyhyi lygyglqtwe
yspeyairsw fyialhavpg flarglglslr lhfvyfirgv lacfsafcet nlilavarnf
nravalhlts vlfvnsgmws astsfllpssf amnmvtlals aqlsppstkr tvkvvsfity
gavigwpfsa alsipfille lvdllkgrfrh lfcwrfkaif vallitgici tvdlslyhri
qfvawnivky nvlakdgrgp diygteppwy yfanlslqhn ivlwfamacg plvllaafn
winldsflldl ssvispfyiw lfifiiqphk eerfmypiyp vlclaaagil dmslklmiqi
lssinetvrs kfpvrffvvc vyaiigclsi arilaiqnyn apmiiypais fletdnnvtt
nvcvgkewyr ypstfflpdn srlkfvksef dgilpgefve snstwnnreg yyqipehmne
fnneeptryt slescdfliid lefdhskstv nepiysksdg wipvmvypfi dtkqtpfmg
afavpfiepk wgyeilvkk pvkidfsnlr raskqqa

FIGURE 8

Enzymatic-depletion/ re-amplification 5'-RACE strategy



Fusion Partner pMT
exon7-8boundary

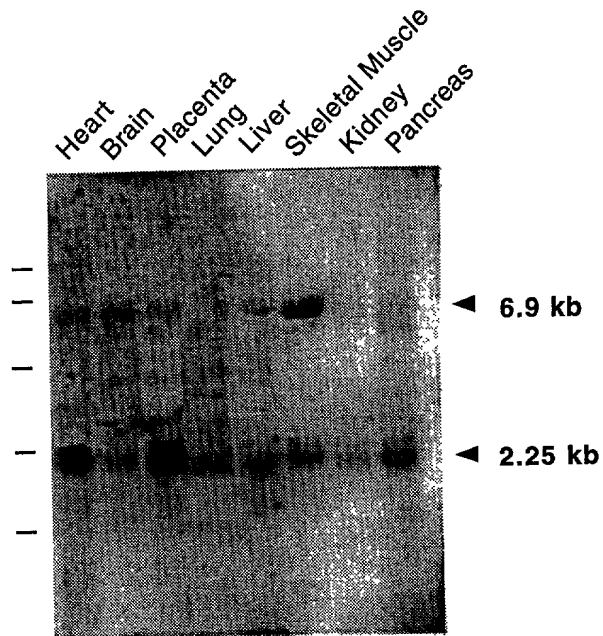
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LCKSQGDDXTCIVPLPSSGKSMEGLLRTSIYPRTFCLWCVPYQNLGHPY

FIGURE 9

Figure 5

Expression Studies

A



B

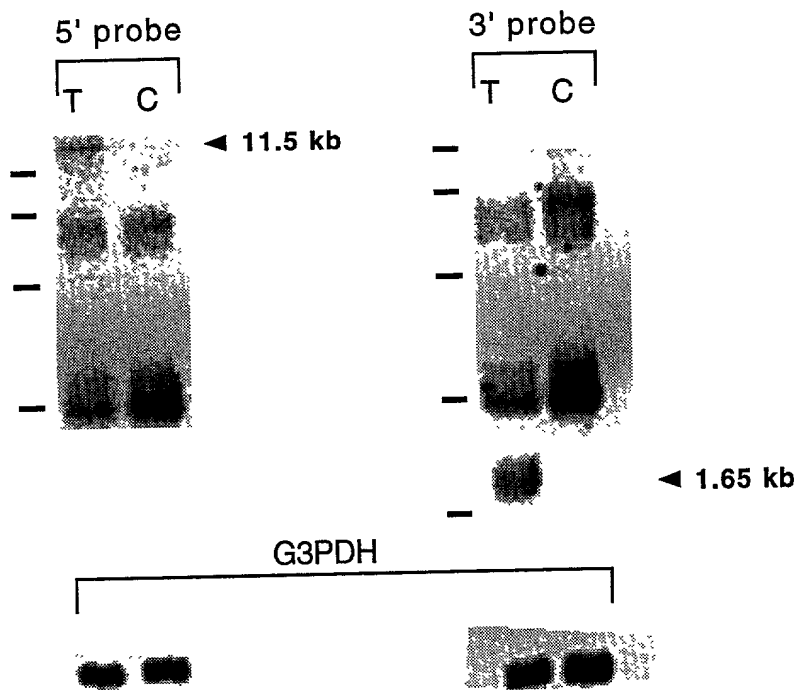


FIGURE 10